

Copyright (C) 1993 - 2005 CompuGen Ltd.

Om protein - nucleic search, using frame_plus_p2n model

Run on: May 27, 2005, 08:52:42 ; Search time 4551 Seconds
 (without alignment(s))
 3788.863 Million cell updates/sec

Title: Perfect score:
Sequence: US-10-054-534B-14
Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
DelPop 6.0 , Delext 7.0

Searched: 3429544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Command line parameters:
 -MOBPL=frame+ P2N.model -DEV=x1h
 -O=cgn2_1 /USP0_spool h/US10054534/runat_26052005_164253_18398/app_query.fasta_1.647
 -DB=EST -QFMT=fasta -MINMATCH=0.1 -LOOPCL=0 -TOPOEXP=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40_cdi -LIST=45
 -OUTFILE=EST -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=US10054534 @CGN 1_1 37 @runat_26052005_164253_18398 -NCPU=6 -ICPU=3
 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THR_BADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELPop=6 -DELEXT=7

Database :

- 1: gb_eat1:*
- 2: gb_eat2:*
- 3: gb_htc:*
- 4: gb_eat3:*
- 5: gb_eat4:*
- 6: gb_eat5:*
- 7: gb_eat6:*
- 8: gb_gb81:*
- 9: gb_gb82:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ⁿ ID	Description
1	571	23.6	1764	AY103762
2	503.5	20.8	1569	CNS0550
3	498.5	20.6	1335	9
4	493.	20.4	1335	9
5	491.	20.4	1335	9
6	486.5	20.1	1946	3
7	485.5	20.1	1521	3
8	485.5	20.1	1530	6
9	485.5	20.1	1641	3

AL512760 Homo sapi

AK083959 Mus muscu

BX025756 Arabidops

CN200461 Tor10137

AK080414 Mus muscu

AK029318 Mus muscu

CR608795 Full-length

AK083822 Mus muscu

AK090042 Mus muscu

AK076485 Mus muscu

CG238209 OG082167

CG364599 OGWM272

CG237761 OGYS487

AY420236 Mus muscu

CR593148 Full-length

AY20234

AY420234 Homo sapi

CG440392 OGTRX947

CG46170 PRJF270

AY420235 Pan trogl

AY418549 Pan trogl

AY202411 Tor2601

AY420234 Homo sapi

CG464523 55-802082

CV198376 CGPR00397

CO18959 GR_Eb021

BR0881930 AGENCOURT

BR687867 BOHSQ94TP

CG449172 OG9AD87H

AK033308 Mus muscu

CD837141 BN45_051D

B0024653 QHFSH12.Y

B0028101 ORGQG05.Y

BU025031 QHFBT24.Y

CO129755 GR_Eb31C

CR018275

BU025281 full-length

BU025281 QHFBK24.Y

BU025987 QHG12J25.

RESULT 1

DEFINITION Zea mays PC0097385 mRNA sequence.

ACCESSION AY103762

VERSION AY103762.1

KEYWORDS HTC

SOURCE Zea mays

ORGANISM Zea mays

Bukaryota; Viscidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCOA; clade; Panicoidae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 1764)

Haley,C.P., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V. Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes Unpublished (2002)

JOURNAL 2 (bases 1 to 1764)

REFERENCE Coe,E.H. Direct Submission

ARTICLE Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

COMMENT If you are interested in getting corresponding physical clones, there are publicly available from ZmDB, which may be found by BLAST searching at MSL, maize.mizzen.org, ZmDB, www.ZmDB.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.ZmDB.iastate.edu.

FEATURES Source

1. 1764

1/organism="Zea mays"

GenCore version 5.1.6
copyright (c) 1993 - 2005 Compugen Ltd.

On protein - nucleic search, using frame_plus_p2n model.
Run on: May 27, 2005, 09:16:26 ; Search time 816 Seconds
(without alignments)
3408.358 Million cell updates/sec

Title: US-10-054-534B-14

Perfect score: 2415

Sequence: 1 MVGOKREKISWATREHNR.....EVVHLERISIEPFKEFPAM 453

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5700845 seqs, 306977957 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-O=/cgn2_1/usipro_spool/h/US10054534/runat_26052005_164255_18483/app_query.fasta_1.647
-DB=published_Applications_NA_QFMT=factap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=Lblosum62
-TRANS=human0.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=fct -THR MAX=100
-THR MIN=0 -ALIGN=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USERID=US10054534 @CGN 1.1 480 @runat_26052005_164255_18483
-NCPU=6 -TCPUR=3 -NO NMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA,*

```

1: /cgn2_1/pctdata/2/pubpna/US07_PUBCCMB.seq:*
2: /cgn2_1/pctdata/2/pubpna/US07_NEW_PUB_seq:*
3: /cgn2_1/pctdata/2/pubpna/US07_PUBCOMB.seq:*
4: /cgn2_1/pctdata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_1/pctdata/2/pubpna/US07_NEW_PUB_seq:*
6: /cgn2_1/pctdata/2/pubpna/US07_PUBCCMB.seq:*
7: /cgn2_1/pctdata/2/pubpna/US08_NEW_PUB_seq:*
8: /cgn2_1/pctdata/2/pubpna/US08_PUBCCMB.seq:*
9: /cgn2_1/pctdata/2/pubpna/US09_PUBCCMB.seq:*
10: /cgn2_1/pctdata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_1/pctdata/2/pubpna/US09_PUBCOMB.seq:*
12: /cgn2_1/pctdata/2/pubpna/US09_PUB seq:*
13: /cgn2_1/pctdata/2/pubpna/US09_PUBCOMB.seq:*
14: /cgn2_1/pctdata/2/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_1/pctdata/2/pubpna/US10_PUBCOMB.seq:*
16: /cgn2_1/pctdata/2/pubpna/US10_PUBCOMB.seq:*
17: /cgn2_1/pctdata/2/pubpna/US10_PUBCOMB.seq:*
18: /cgn2_1/pctdata/2/pubpna/US10_PUBCOMB.seq:*
19: /cgn2_1/pctdata/2/pubpna/US10_NEW_PUB_seq:*
20: /cgn2_1/pctdata/2/pubpna/US11_NEW_PUB_seq:*
21: /cgn2_1/pctdata/2/pubpna/US60_NEW_PUB_seq:*
22: /cgn2_1/pctdata/2/pubpna/US60_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2415	100.0	1362	10 US-09-719-862-13	Sequence 13, Appl
2	2415	100.0	1362	15 US-10-431-952-13	Sequence 13, Appl
3	2415	100.0	1362	16 US-10-471-951-13	Sequence 13, Appl
4	2415	100.0	1362	18 US-10-776-311-35	Sequence 35, Appl
5	1537	63.0	1380	9 US-09-967-477-27	Sequence 7, Appl
6	1129.5	46.8	1434	17 US-10-230-821-3	Sequence 3, Appl
7	1129.5	46.8	1434	17 US-10-230-552-3	Sequence 3, Appl
8	943	39.0	1374	15 US-10-278-391-3	Sequence 3, Appl
9	943	39.0	1374	18 US-10-840-471-1	Sequence 1, Appl
10	943	39.0	1374	18 US-10-840-471-25	Sequence 25, Appl
11	943	39.0	1617	18 US-10-776-311-33	Sequence 35, Appl
12	943	39.0	10328	19 US-10-840-322-129	Sequence 33, Appl
13	943	39.0	8894	19 US-10-840-325-124	Sequence 129, Appl
14	922.5	38.2	1578	17 US-10-260-821-7	Sequence 7, Appl
15	758	31.4	1578	17 US-10-230-553-7	Sequence 7, Appl
16	758	31.4	15430	17 US-10-230-821-25	Sequence 25, Appl
17	758	31.4	15430	17 US-10-250-552-25	Sequence 25, Appl
18	758	31.4	17752	17 US-10-230-821-28	Sequence 28, Appl
19	758	31.4	17752	17 US-10-230-553-28	GENERAL INFORMATION
20	758	31.4	17752	17 US-10-230-553-28	Sequence 83761, A
21	570.5	23.6	1944	18 US-10-437-963-83751	Sequence 15122, A
22	565.5	23.4	2144	17 US-10-425-114-15122	Sequence 59986, A
23	565.5	23.4	2356	17 US-10-424-599-5986	Sequence 2088, APP
24	565.5	23.4	2054	17 US-10-329-566-288	Sequence 2, Appl
25	561.5	23.3	1344	16 US-10-320-772-2	Sequence 18, Appl
26	557.5	23.3	168	17 US-10-230-821-18	Sequence 18, Appl
27	557.5	23.1	648	17 US-10-230-553-18	Sequence 149471, A
28	551	22.8	2236	17 US-10-424-599-124471	Sequence 26, Appl
29	547	22.7	167	17 US-10-425-114-14991	Sequence 26, Appl
30	535	22.2	1702	13 US-10-039-756-26	Sequence 26, Appl
31	535	22.2	1702	17 US-10-702-777-26	Sequence 26, Appl
32	528.5	21.9	1685	17 US-10-029-754-4	Sequence 4, Appl
33	528.5	21.9	1685	17 US-10-702-777-4	Sequence 4, Appl
34	522.5	21.6	1350	9 US-09-931-8424-558	Sequence 558, APP
35	522.5	21.6	1350	11 US-09-931-8424-558	Sequence 14869, A
36	522.5	21.6	1828	17 US-10-425-114-14869	Sequence 3353, AP
37	522.5	21.6	1883	18 US-10-739-930-3353	Sequence 36789, A
38	522.5	21.6	1940	17 US-10-424-599-36789	Sequence 83759, A
39	513.5	21.3	1302	18 US-10-427-963-83759	Sequence 3, Appl
40	512.5	21.2	1362	19 US-10-574-422-3	Sequence 879, APP
41	510.5	21.1	1503	19 US-10-577-795-879	Sequence 1, Appl
42	500.5	20.7	1362	19 US-10-574-422-1	Sequence 4, Appl
43	498.5	20.6	1335	17 US-10-239-6528-4	Sequence 1010, AP
44	498.5	20.6	3015	17 US-10-429-6528-5	Sequence 1010, AP
45	498.5	20.6	3149	17 US-10-172-118-1010	Sequence 1010, AP

ALIGNMENTS

RESULT 1
US-09-769-863-13
Sequence 13, Application US/09769863

Publication No. US20030151441
GENERAL INFORMATION:

APPLICANT: Abbott Laboratories
APPLICANT: Mukerji Pradip
APPLICANT: Huang, Yung Sheng
APPLICANT: Das, Tapas
APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.

TITLE OF INVENTION: DESARTANSE GENES AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/769,863

CURRENT FILING DATE: 2001-01-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 13

LENGTH: 1362

TYPE: DNA

GenCore version 5.1.6
Copyright (C) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 27, 2005, 08:55:06 ; Search time 249 Seconds
(w/out alignments)
2976.841 Million cell updates/sec

Title: Perfect score: US-10-054-534B-14

Sequence: 1 MNGQKAKRISMATIREHNR.EVVWHIERSISRFKRFAM 453

Scoring table: BLOSUM62

Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5
Fgapop 6.0	Fgapext 7.0
DelOp 6.0	Delect 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MQBBL=frame+p2n.model -DEV=jdb
-Q=/cgn2_1/USPRO_spool/h/US10054534/runat_26052005_164253_18411/app_query.fasta_1.647
-DB=issued_patents_na -QMT=fastap -SURPRX=rml -MNTMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human0.cdi
-LIST=5 -DOALIGN=000 -THR SCORE=PCT -THR MAX=0 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=PTO -NORMEXT -HEARPE=500 -MLNLEN=0 -MAXLEN=200000000
-USER=US10054534 @CNCN 1 1 69 0 runat_26052005_164253_18411 -NCPU=6 -ICLU=3
-NO MMAB -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-RGAPEXT=7 -YEARPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
-MQBBL=frame+p2n.model -DEV=jdb
-Q=/cgn2_1/USPRO_spool/h/US10054534/runat_26052005_164253_18411/app_query.fasta_1.647
-DB=issued_patents_na -QMT=fastap -SURPRX=rml -MNTMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human0.cdi
-LIST=5 -DOALIGN=000 -THR SCORE=PCT -THR MAX=0 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=PTO -NORMEXT -HEARPE=500 -MLNLEN=0 -MAXLEN=200000000
-USER=US10054534 @CNCN 1 1 69 0 runat_26052005_164253_18411 -NCPU=6 -ICLU=3
-NO MMAB -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-RGAPEXT=7 -YEARPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/PCFUUS_COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2415	100.0	1362	4 US-09-769-863-13
2	943	39.0	1617	2 US-08-634-655-1
3	943	39.0	1617	3 US-08-834-033A1
4	943	39.0	1617	3 US-09-363-574-1
5	943	39.0	1617	3 US-09-363-576-1
6	943	39.0	1617	3 US-09-330-235-17
7	641.5	1281	4 US-09-857-503B-3	
8	561.5	2333	4 US-09-651-4	
9	535	22.2	1702	3 US-08-934-254-26
10	535	22.2	1702	4 US-09-685-775-26
11	528.5	21.9	1684	2 US-08-831-570-1
12	528.5	21.9	1684	2 US-08-831-575-1

ALIGNMENTS

RESULT	SEQUENCE ID	TYPE	LENGTH	ORGANISM
1	US-09-769-863-13	DNA	1362	Saprolegnia diclina

US-09-769-863-13

Alignment Scores:

Pred. No. :	1.77e-299	Length: 1362
Score: 2415.00	Matches: 453	
Percent Similarity: 10.00%	Conservative: 0	
Best Local Similarity: 10.00%	Mismatches: 0	
Query Match: 10.00%	Indels: 0	
DB: 4	Gaps: 0	

US-10-054-534B-14 (1-453) x US-09-769-863-13 (1-1362)

QY

1	MetValGlnGlyGlnAlaGluValAspSerTnPAlaThrLeuArgGluHisArg
Db	1 ATGGTCAGGGCAAGGCCGAGATCTGCGCGACCATCGTGAACTACCCG

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: May 27, 2005, 08:48:31 ; Search time 759 Seconds
(without alignments)
3533.126 Million cell updates/sec

Title: US-10-054-534B-14

Perfect score: 2415

Sequence: 1 MVQGQKAEKISWATIREHNR.....EVVVLHLRISIBFFKEFPAM 453

Scoring table: BLOSUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delex	7.0

Searched: 4398206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+P2N.model -DEV=1h
-Q//cgn2_1/USPOOL/spool_h/US10054534/runat_26052005_164252_18381/app/query.fasta_1.647
-DB=N Geneseq -OPFM=faster -SUFFIX=runat -MINMATCH=1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -SPART=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLOG=- -DOCGF=200 -THR SCOREPCT= -THR MAX=100 -THR MIN=0 -ALIGNAL=15 -MODE=LOCAL
-OUTFMT=sto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=000000000
-USER=US10054534 @CEN_1..1..70 @unat_26052005_164252_18381 -NCPU=6 -ICPU=3
-NO_MMW -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
:FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEX=7

Database : N_Genesed_16Dec04:**

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003bs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT	1
ID	AAD49064 standard; DNA; 1362 BP.
XX	AC
XX	AAD49064;
XX	DT 07-MAR-2003 (first entry)
XX	Saprolegnia diclina delta 6 desaturase DNA.
DE	
XX	Delta 5 desaturase; delta 6 desaturase; polyunsaturated fatty acid; PUFA; angioedema; osteoporosis; inflammation; rheumatoid arthritis; psoriasis; premenstrual syndrome; myalgic encephalitis; chronic fatigue; vasotropin; acquired immune deficiency syndrome; AIDS; multiple sclerosis; virucide; osteopathic; litholytic; nephrotropic; neuroprotective; anticoagulant; therapy; antilipemic; hypotensive; kidney stone; cachexia; cytostatic; eczema; cancer; asthma; enzyme; gene; ds.
OS	saprolegnia diclina.
XX	
PH	:key
FT	CDS
FT	1 .1362 /tag= a
FT	/product= "saprolegnia diclina delta 6 desaturase"
XX	Aad49064 Saprolegnia Adt20162 Saprolegnia Aad5090 Pythium i. Abv74258 Phaeodactylus Abq76780 P. tricornis
XX	W0200281668-A2.
PD	17-OCT-2002.
XX	

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2415	100.0	1362 8 AAD49064	Aad49064 Saprolegnia Adt20162 Saprolegnia Aad5090 Pythium i. Abv74258 Phaeodactylus Abq76780 P. tricornis
2	2415	100.0	1362 13 ADR20162	
3	1537	63.6	1380 6 AAD35090	
4	1129.5	46.8	1434 6 ADR74258	
5	1129.5	46.8	1434 6 ABQ76780	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: May 27, 2005, 08:49:06 ; Search time 6201 Seconds
(without alignments)

3539.786 Million cell updates/sec

Title: US-10-054-534B-14
Perfect score: 2415
Sequence: 1 MVQGOKAKISWATIRENR.....EVVVLHLRISIEFFKSFPPAM 453

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext: 0.5
Ygapop 10.0 , Ygapext: 0.5
Pgapop 6.0 , Pgapext: 7.0
Delop 6.0 , Delext: 7.0

Searched: 4708233 seqs, 24227670755 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 10‡

Listing first 45 summaries

Command line parameters:
-MODEL:frame,-p2n.model -DEV=xlh
-Q-/cgn2.1/USPETO_spool/h/US10054534/runat_26052005_164252_18387/app_query.fasta_1.647
-DB=GenEmbl -QFMRFastap -TRANS=blosum62 -MINMATCH=0.1 -LOOPCFL=0 -LOOPEXT=0
-UNITS=bit -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=99 -THR MAX=100 -THR MIN=0 -ALIGN=40
-OUTPMT_PTO -NORM=EXT -HEAPSIZE=500 -MINTLEN=0 -MAXLEN=200000000
-USER=US10054534 @CGN 1_1 3731 @runat_26052005_164252_1687 -NPNU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DEPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:
1: gb_ba:
2: gb_ntg:
3: gb_in:
4: gb_on:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pi:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
AR410195 LOCUS AR410195 DEFINITION Sequence 13 from patent US 6635451. DNA linear PAT 18-DEC-2003

DEFINITION Sequence 13 from patent US 6635451.
ACCESSION AR410195
VERSION AR410195.1 GI:40161436
KEYWORDS SOURCE ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 1362)
AUTHORS Mukerji,P., Huang,Y.-S., Das,T., Thurmond,J. and Pereira,S.L.
TITLE Desaturase genes and uses thereof
JOURNAL Patent: US 6635451-A 13-21-OCT-2003;
FEATURES Location/Qualifiers 1. .1362
ORIGIN Source /organism="unknown"
/mol_type="genomic DNA"

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2415	100.0	1362	6 AR410195 Sequence
2	2415	100.0	1362	6 AX576988 Sequence
3	1537	63.6	1380	6 AX467717 Sequence
4	1537	63.6	1380	8 AF419296 Pythium i

				GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.				
run on:				May 27, 2005, 05:35:03 ; Search time 388 Seconds
protein - protein search, using sw model				(without alignments)
sequence:				597.866 Million cell updates/sec
perfect score:				US-10-054-534B-14
title:				1 MVQGQAKRISWATIREHNR.....EVVHLERISIEFFKFPAM 453
searched:				
scoring table:				BLOSUM62
gapopen:				Gapext 0.5
database :				1612378 seqs, 512079187 residues
result No.	Score	Query Match Length	DB ID	
1	1537	63 6	459	2 Q944W4
2	1129.5	46 8	477	2 Q8RBU0
3	94.5	39 1	457	2 Q8UUV3
4	943	39 0	457	2 Q8UUV3
5	94.0	38 9	457	2 Q8XJ73
6	938	38 8	457	2 Q8Y4P4
7	937	38 8	457	2 Q7BL2
8	932	38 6	458	2 Q7LWB
9	921	38 1	457	2 Q8XJ74
10	917	38 0	457	2 Q9HEY1
11	900	37 3	458	2 Q7SP62
12	900	37 3	458	2 Q7Z8P2
13	822.5	34 1	481	2 Q96VB8
14	818	33 9	467	2 Q96VC3
15	817	33 8	520	2 Q9LEM9
16	817	33 8	520	2 Q9LEM9
17	798.5	33 1	483	2 Q9IENO
18	785.5	32 5	671V28	
19	779.5	32 3	357	2 Q9HDF4
20	758	31 4	525	2 Q9ZMW2
21	613	25 4	419	2 QSWWQ9
22	586.5	24 3	443	2 Q3221
23	585.5	24 2	443	2 Q61388
24	561.5	23 6	447	2 Q9XTB7
25	558.5	23 1	458	2 Q33469
26	558	23 1	446	2 Q8LBD7
27	549	22 7	469	2 Q9ZTUB
28	533.5	22 1	464	2 Q636V5
29	532	22 0	446	2 Q71BG3
30			2 Q71BG4	
31				
32				530.5 22.0 448 2 Q8VZZ1
33				529.5 21.9 448 2 Q8VZZ2
34				528.5 21.9 448 2 Q8SAUS
35				527.5 21.8 448 2 Q04353
36				523 21.7 446 2 Q9ZTY9
37				522.5 21.6 449 2 Q9ZRP7
38				521.5 21.6 449 2 Q9ZRP8
39				518.5 21.5 449 2 Q8LB96
40				513.5 21.3 453 2 Q84KG6
41				509.5 21.1 452 2 Q84KG9
42				503 20.8 446 2 Q6DDK2
43				502.5 20.8 452 2 Q84KG7
44				500.5 20.7 453 2 Q84KG8
45				500 20.7 444 1 FADS_BRARE
46				
47				
48				
49				
50				
51				
52				
53				
54				
55				
56				
57				
58				
59				
60				
61				
62				
63				
64				
65				
66				
67				
68				
69				
70				
71				
72				
73				
74				
75				
76				
77				
78				
79				
80				
81				
82				
83				
84				
85				
86				
87				
88				
89				
90				
91				
92				
93				
94				
95				
96				
97				
98				
99				
100				
101				
102				
103				
104				
105				
106				
107				
108				
109				
110				
111				
112				
113				
114				
115				
116				
117				
118				
119				
120				
121				
122				
123				
124				
125				
126				
127				
128				
129				
130				
131				
132				
133				
134				
135				
136				
137				
138				
139				
140				
141				
142				
143				
144				
145				
146				
147				
148				
149				
150				
151				
152				
153				
154				
155				
156				
157				
158				
159				
160				
161				
162				
163				
164				
165				
166				
167				
168				
169				
170				
171				
172				
173				
174				
175				
176				
177				
178				
179				
180				
181				
182				
183				
184				
185				
186				
187				
188				
189				
190				
191				
192				
193				
194				
195				
196				
197				
198				
199				
200				
201				
202				
203				
204				
205				
206				
207				
208				
209				
210				
211				
212				
213				
214				
215				
216				
217				
218				
219				
220				
221				
222				
223				
224				
225				
226				
227				
228				
229				
230				
231				
232				
233				
234				
235				
236				
237				
238				
239				
240				
241				
242				
243				
244				
245				
246				
247				
248				
249				
250				
251				
252				
253				
254				
255				
256				
257				
258				
259				
260				
261				
262				
263				
264				
265				
266				
267				
268				
269				
270				
271				
272				
273				
274				
275				
276				
277				
278				
279				
280				
281				
282				
283				
284				
285				
286				
287				
288				
289				
290				
291				
292				
293				
294				
295				
296				
297				
298				
299				
300				
301				
302				
303				
304				
305				
306				
307				
308				
309				
310				
311				
312				
313				
314				
315				
316				
317				
318				
319				
320				
321				
322				
323				
324				
325				
326				
327				
328				
329				
330				
331				
332				
333				
334				
335				
336				
337				
338				
339				
340				
341				
342				
343				
344				
345				
346				
347				
348				
349				
350				
351				
352				
353				
354				
355				
356				
357				
358				
359				
360				
361				
362				
363				
364				
365				
366				
367				
368				
369				
370				
371				
372				
373				
374				
375				
376				
377				
378				
379				
380				
381				
382				
383				
384				
385				
386				
387				

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2005, 08:47:10 ; Search time 468 Seconds
 (without alignment)

333.916 Million cell updates/sec

Title:	US-10-054-534B-14
Perfect score:	2415
Sequence:	1 MVOQKAKRISWATIREHNR.EWWVHLERISIEPERKEFPM 453
Scoring table:	BLOSUM62
Gapop 10.0 , Gapext 0.5	
Searched:	1462999 seqs, 344972447 residues
Total number of hits satisfying chosen parameters:	1462099
Minimum DB seq length:	0
Maximum DB seq length:	200000000
Post-processing:	Minimum Match 0%
Maximum Match 100%	
Listing first 45 summaries	
Database :	Published Applications AA: *
1:	/cgn2_6/pctodata/2/pubpaa/US08_PUBCOMB.pep: *
2:	/cgn2_6/pctodata/2/pubpaa/PCT_NEW_PUB.pep: *
3:	/cgn2_6/pctodata/2/pubpaa/US06_NEW_PUB.pep: *
4:	/cgn2_6/pctodata/2/pubpaa/US06_PUBCOMB.pep: *
5:	/cgn2_6/pctodata/2/pubpaa/US07_NEW_PUB.pep: *
6:	/cgn2_6/pctodata/2/pubpaa/PCTUS_PUBCOMB.pep: *
7:	/cgn2_6/pctodata/2/pubpaa/US08_NEW_PUB.pep: *
8:	/cgn2_6/pctodata/2/pubpaa/US08_PUBCOMB.pep: *
9:	/cgn2_6/pctodata/2/pubpaa/US09_PUBCOMB.pep: *
10:	/cgn2_6/pctodata/2/pubpaa/US095_PUBCOMB.pep: *
11:	/cgn2_6/pctodata/2/pubpaa/US09C_PUBCOMB.pep: *
12:	/cgn2_6/pctodata/2/pubpaa/US10_PUBCOMB.pep: *
13:	/cgn2_6/pctodata/2/pubpaa/US10A_PUBCOMB.pep: *
14:	/cgn2_6/pctodata/2/pubpaa/US10B_PUBCOMB.pep: *
15:	/cgn2_6/pctodata/2/pubpaa/US10C_PUBCOMB.pep: *
16:	/cgn2_6/pctodata/2/pubpaa/US10D_PUBCOMB.pep: *
17:	/cgn2_6/pctodata/2/pubpaa/US11_NEW_PUB.pep: *
18:	/cgn2_6/pctodata/2/pubpaa/US11_NEW_PUB.pep: *
19:	/cgn2_6/pctodata/2/pubpaa/US60_NEW_PUB.pep: *
20:	/cgn2_6/pctodata/2/pubpaa/US60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2415	100.0	453	10 US-09-769-863-14
2	2415	100.0	453	14 US-10-054-534B-14
3	2415	100.0	453	14 US-10-431-952-14
4	2415	100.0	453	16 US-10-776-311-36
5	1537	63.6	459	9 US-09-667-477B-8
6	1129.5	46.8	477	15 US-10-250-821-4
7	1129.5	46.8	477	15 US-10-250-553-4
8	943	39.0	457	14 US-10-278-391-4
9	943	39.0	457	16 US-10-776-311-34
10	943	39.0	457	17 US-10-840-325-37
11	943	39.0	458	14 US-10-191-513A-11
12	943	39.0	458	14 US-10-191-513A-41
13	758	31.4	525	15 US-10-250-821-8

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2415	100.0	453	10 US-09-769-863-14
2	2415	100.0	453	14 US-10-054-534B-14
3	2415	100.0	453	14 US-10-431-952-14
4	2415	100.0	453	16 US-10-776-311-36
5	1537	63.6	459	9 US-09-667-477B-8
6	1129.5	46.8	477	15 US-10-250-821-4
7	1129.5	46.8	477	15 US-10-250-553-4
8	943	39.0	457	14 US-10-278-391-4
9	943	39.0	457	16 US-10-776-311-34
10	943	39.0	457	17 US-10-840-325-37
11	943	39.0	458	14 US-10-191-513A-11
12	943	39.0	458	14 US-10-191-513A-41
13	758	31.4	525	15 US-10-250-821-8

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2415	100.0	453	10 US-09-769-863-14
2	2415	100.0	453	14 US-10-054-534B-14
3	2415	100.0	453	14 US-10-431-952-14
4	2415	100.0	453	16 US-10-776-311-36
5	1537	63.6	459	9 US-09-667-477B-8
6	1129.5	46.8	477	15 US-10-250-821-4
7	1129.5	46.8	477	15 US-10-250-553-4
8	943	39.0	457	14 US-10-278-391-4
9	943	39.0	457	16 US-10-776-311-34
10	943	39.0	457	17 US-10-840-325-37
11	943	39.0	458	14 US-10-191-513A-11
12	943	39.0	458	14 US-10-191-513A-41
13	758	31.4	525	15 US-10-250-821-8

SUMMARIES

RESULT: 1
 US-09-769-863-14
 Sequence 14, Appli
 Publication No. US/09769863
 GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories
 APPLICANT: Mukerji, Pradip
 APPLICANT: Huang, Yung-Sheng
 APPLICANT: Das, Tapas
 APPLICANT: Thurmond, Jennifer
 APPLICANT: Pereira, Suzette L.
 TITLE OF INVENTION: DISASTURASE GENES AND USES THEREOF
 RULE REFERENCE: 6763 US-01
 CURRENT APPLICATION NUMBER: US/09769,863
 CURRENT FILING DATE: 2001-01-25
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 14
 LENGTH: 453
 TYPE: PRT
 ORGANISM: Saprolegnia diclina

Query Match
 Best Local Similarity 100.0%; Score 2415; DB 10; Length 453;
 Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MVOQKAKRISWATIREHNR.EWWVHLERISIEPERKEFPM 453
Qy	1	MVOQKAKRISWATIREHNR.EWWVHLERISIEPERKEFPM 453
Qy	1	MVOQKAKRISWATIREHNR.EWWVHLERISIEPERKEFPM 453

Sequence 27, Appli
 Sequence 30, Appli
 Sequence 8, Appli
 Sequence 27, Appli
 Sequence 20, Appli
 Sequence 186242, Appli
 Sequence 19, Appli
 Sequence 19, Appli
 Sequence 267313, Appli
 Sequence 4, Appli
 Sequence 6107, Appli
 Sequence 447, Appli
 Sequence 11, Appli
 Sequence 19, Appli
 Sequence 19, Appli
 Sequence 267313, Appli
 Sequence 4, Appli
 Sequence 5, Appli
 Sequence 5, Appli
 Sequence 17963, Appli
 Sequence 52563, Appli
 Sequence 27, Appli
 Sequence 13, Appli
 Sequence 4, Appli
 Sequence 5, Appli
 Sequence 5, Appli
 Sequence 26, Appli
 Sequence 7, Appli
 Sequence 8, Appli
 Sequence 9, Appli

ALIGNMENTS

RESULT: 1
 US-09-769-863-14
 Sequence 14, Application US/09769863

Publication No. US/09769863

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Mukerji, Pradip

APPLICANT: Huang, Yung-Sheng

APPLICANT: Das, Tapas

APPLICANT: Thurmond, Jennifer

APPLICANT: Pereira, Suzette L.

TITLE OF INVENTION: DISASTURASE GENES AND USES THEREOF

RULE REFERENCE: 6763 US-01

CURRENT APPLICATION NUMBER: US/09769,863

CURRENT FILING DATE: 2001-01-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14

LENGTH: 453

TYPE: PRT

ORGANISM: Saprolegnia diclina

Query Match
 Best Local Similarity 100.0%; Score 2415; DB 10; Length 453;
 Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MVOQKAKRISWATIREHNR.EWWVHLERISIEPERKEFPM 453
Qy	1	MVOQKAKRISWATIREHNR.EWWVHLERISIEPERKEFPM 453
Qy	1	MVOQKAKRISWATIREHNR.EWWVHLERISIEPERKEFPM 453

Sequence 27, Appli
 Sequence 30, Appli
 Sequence 8, Appli
 Sequence 27, Appli
 Sequence 20, Appli
 Sequence 186242, Appli
 Sequence 19, Appli
 Sequence 19, Appli
 Sequence 267313, Appli
 Sequence 4, Appli
 Sequence 4, Appli
 Sequence 5, Appli
 Sequence 5, Appli
 Sequence 17963, Appli
 Sequence 52563, Appli
 Sequence 27, Appli
 Sequence 13, Appli
 Sequence 4, Appli
 Sequence 5, Appli
 Sequence 5, Appli
 Sequence 26, Appli
 Sequence 7, Appli
 Sequence 8, Appli
 Sequence 9, Appli

ALIGNMENTS

RESULT: 1
 US-09-769-863-14
 Sequence 14, Application US/09769863

Publication No. US/09769863

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Mukerji, Pradip

APPLICANT: Huang, Yung-Sheng

APPLICANT: Das, Tapas

APPLICANT: Thurmond, Jennifer

APPLICANT: Pereira, Suzette L.

TITLE OF INVENTION: DISASTURASE GENES AND USES THEREOF

RULE REFERENCE: 6763 US-01

CURRENT APPLICATION NUMBER: US/09769,863

CURRENT FILING DATE: 2001-01-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14

LENGTH: 453

TYPE: PRT

ORGANISM: Saprolegnia diclina

Query Match
 Best Local Similarity 100.0%; Score 2415; DB 10; Length 453;
 Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MVOQKAKRISWATIREHNR.EWWVHLERISIEPERKEFPM 453
Qy	1	MVOQKAKRISWATIREHNR.EWWVHLERISIEPERKEFPM 453
Qy	1	MVOQKAKRISWATIREHNR.EWWVHLERISIEPERKEFPM 453

Sequence 27, Appli
 Sequence 30, Appli
 Sequence 8, Appli
 Sequence 27, Appli
 Sequence 20, Appli
 Sequence 186242, Appli
 Sequence 19, Appli
 Sequence 19, Appli
 Sequence 267313, Appli
 Sequence 4, Appli
 Sequence 4, Appli
 Sequence 5, Appli
 Sequence 5, Appli
 Sequence 17963, Appli
 Sequence 52563, Appli
 Sequence 27, Appli
 Sequence 13, Appli
 Sequence 4, Appli
 Sequence 5, Appli
 Sequence 5, Appli
 Sequence 26, Appli
 Sequence 7, Appli
 Sequence 8, Appli
 Sequence 9, Appli

ALIGNMENTS

RESULT: 1
 US-09-769-863-14
 Sequence 14, Application US/09769863

Publication No. US/09769863

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Mukerji, Pradip

APPLICANT: Huang, Yung-Sheng

APPLICANT: Das, Tapas

APPLICANT: Thurmond, Jennifer

APPLICANT: Pereira, Suzette L.

TITLE OF INVENTION: DISASTURASE GENES AND USES THEREOF

RULE REFERENCE: 6763 US-01

CURRENT APPLICATION NUMBER: US/09769,863

CURRENT FILING DATE: 2001-01-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14

LENGTH: 453

TYPE: PRT

ORGANISM: Saprolegnia diclina

Query Match
 Best Local Similarity 100.0%; Score 2415; DB 10; Length 453;
 Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MVOQKAKRISWATIREHNR.EWWVHLERISIEPERKEFPM 453
Qy	1	MVOQKAKRISWATIREHNR.EWWVHLERISIEPERKEFPM 453
Qy	1	MVOQKAKRISWATIREHNR.EWWVHLERISIEPERKEFPM 453

Sequence 27, Appli
 Sequence 30, Appli
 Sequence 8, Appli
 Sequence 27, Appli
 Sequence 20, Appli
 Sequence 186242, Appli
 Sequence 19, Appli
 Sequence 19, Appli
 Sequence 267313, Appli
 Sequence 4, Appli
 Sequence 4, Appli
 Sequence 5, Appli
 Sequence 5, Appli
 Sequence 17963, Appli
 Sequence 52563, Appli
 Sequence 27, Appli
 Sequence 13, Appli
 Sequence 4, Appli
 Sequence 5, Appli
 Sequence 5, Appli
 Sequence 26, Appli
 Sequence 7, Appli
 Sequence 8, Appli
 Sequence 9, Appli

ALIGNMENTS

RESULT: 1
 US-09-769-863-14
 Sequence 14, Application US/09769863

Publication No. US/09769863

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Mukerji, Pradip

APPLICANT: Huang, Yung-Sheng

APPLICANT: Das, Tapas

APPLICANT: Thurmond, Jennifer

APPLICANT: Pereira, Suzette L.

TITLE OF INVENTION: DISASTURASE GENES AND USES THEREOF

RULE REFERENCE: 6763 US-01

CURRENT APPLICATION NUMBER: US/09769,863

CURRENT FILING DATE: 2001-01-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14

LENGTH: 453

TYPE: PRT

ORGANISM: Saprolegnia diclina

Query Match
 Best Local Similarity 100.0%; Score 2415; DB 10; Length 453;
 Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MVOQKAKRISWATIREHNR.EWWVHLERISIEPERKEFPM 453
Qy	1	MVOQKAKRISWATIREHNR.EWWVHLERISIEPERKEFPM 453
Qy	1	MVOQKAKRISWATIREHNR.EWWVHLERISIEPERKEFPM 453

Sequence 27, Appli
 Sequence 30, Appli
 Sequence 8, Appli
 Sequence 27, Appli
 Sequence 20, Appli
 Sequence 186242, Appli
 Sequence 19, Appli
 Sequence 19, Appli
 Sequence 267313, Appli
 Sequence 4, Appli
 Sequence 4, Appli
 Sequence 5, Appli
 Sequence 5, Appli
 Sequence 17963, Appli
 Sequence 52563, Appli
 Sequence 27, Appli
 Sequence 13, Appli
 Sequence 4, Appli
 Sequence 5, Appli
 Sequence 5, Appli
 Sequence 26, Appli
 Sequence 7, Appli
 Sequence 8, Appli
 Sequence 9, Appli

ALIGNMENTS

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2005, 05:30:42 ; Search time 318 Seconds
 (without alignments)

55.951 Million cell updates/sec

Title: US-10-054-534B-14
 Perfect score: 2415
 Sequence: 1 MVQGQKAEKISWATIREHNR.....EVVVLHLERISIBPFKSFPPAM 453

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext: 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseq1980s:*
- 2: geneseq1990s:*
- 3: geneseq2000s:*
- 4: geneseq2001s:*
- 5: geneseq2002s:*
- 6: geneseq2003as:*
- 7: geneseq2003bs:*
- 8: geneseq2004gs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	2415	100.0	453	Aae31900
2	2415	100.0	453	ADR20163
3	1537	63.6	459	Aae22063
4	1129.5	46.8	477	ABP98275
5	1129.5	46.8	477	ABG73600
6	1129.5	46.8	477	ADR49338
7	1129.5	46.8	477	ADR49342
8	943	39.0	457	AAW8137
9	943	39.0	457	AAW95504
10	943	39.0	457	AAW95121
11	943	39.0	457	AY556045
12	943	39.0	457	AY92599
13	943	39.0	457	AAB1684
14	943	39.0	457	ADR20161
15	943	39.0	458	ABG9527
16	943	39.0	458	ABG9509
17	943	39.0	458	ABG94707
18	943	39.0	458	ABG94693
19	818	33.9	467	ABP98479
20	817	33.8	467	ABR46440
21	798.5	33.1	483	AB46436
22	798.5	33.1	483	AB46435
23	775.5	32.1	355	ABW8139
24	758	31.4	525	AY51354
25	31.4	525	4	AAB46810

26	758	31.4	525	5	ABB98277
27	758	31.4	525	5	ABG73602
28	758	31.4	525	5	ABG73607
29	758	31.4	525	5	ABG73608
30	758	31.4	525	8	ADR49326
31	758	31.4	525	8	ADR49315
32	713.5	29.5	323	5	ABG96515
33	713.5	29.5	323	5	ABG96698
34	631.5	26.1	421	8	ADP87981
35	619.5	25.7	422	3	ARY96722
36	585.5	24.2	443	2	AYV1751
37	571	23.6	462	3	AYV1552
38	567.5	23.5	473	3	AY51353
39	567.5	23.5	473	8	ADN23455
40	565	23.4	515	8	ADJ48443
41	561.5	23.3	447	2	AYZ1891
42	561.5	23.3	447	3	AYY98721
43	561.5	23.3	447	3	AYY98787
44	558.5	23.1	458	3	AAY51348
45	558.5	23.1	458	7	ADF69394

Result No.	Score	Query Match Length	DB ID	Description
1	2415	100.0	453	Aae31900
2	2415	100.0	453	ADR20163
3	1537	63.6	459	Aae22063
4	1129.5	46.8	477	ABP98275
5	1129.5	46.8	477	ABG73600
6	1129.5	46.8	477	ADR49338
7	1129.5	46.8	477	ADR49342
8	943	39.0	457	AAW8137
9	943	39.0	457	AAW95504
10	943	39.0	457	AAW95121
11	943	39.0	457	AY556045
12	943	39.0	457	AY92599
13	943	39.0	457	AAB1684
14	943	39.0	457	ADR20161
15	943	39.0	458	ABG9527
16	943	39.0	458	ABG9509
17	943	39.0	458	ABG94707
18	943	39.0	458	ABG94693
19	818	33.9	467	ABP98479
20	817	33.8	467	ABR46440
21	798.5	33.1	483	AB46436
22	798.5	33.1	483	AB46435
23	775.5	32.1	355	ABW8139
24	758	31.4	525	AY51354
25	31.4	525	4	AAB46810

The invention relates to delta 5 desaturase or delta 6 desaturase polypeptides and their nucleic acids. These sequences are useful for producing polyunsaturated fatty acids (PUFA) by desaturating PUFA at carbon 5 and carbon 6. Composition comprising at least one PUFA is useful for preventing or treating a condition caused by insufficient intake of PUFA. It is useful for treating restenosis after angioplasty, symptoms of

Copyright (c) 1993 - 2005 Compugen Ltd.

Gencore version 5.1.6

Om nucleic - nucleic search, using sw model
Run on: May 27, 2005, 00:44:37 ; Search time 8715 Seconds
(Without alignments)
5948.771 Million cell updates/sec

Title: US-10-054-534B-13
Perfect score: 1362

Sequence: 1 atggccaggggaaaaaggc.....aggagttcccgccatgtaa 1362

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_htc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gbs1:
9: gb_gbs2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
C 1	96	7.0	819	BUT45135 CHI#007_D
C 2	93.6	6.9	458	CN006019_1:37F09:9
C 3	93.6	6.9	600	CK998942 ip7T09_b
C 4	93	6.8	390	AW026255
C 5	92.8	6.8	509	4 BG68740 307418 MA
C 6	92.6	6.8	884	5 BQ81930
C 7	92	6.8	614	5 BP161817
C 8	91.4	6.7	421	4 CF140245
C 9	91.4	6.7	530	2 AW246354
C 10	91.4	6.7	535	2 BF207014
C 11	91.4	6.7	581	5 BP252288
C 12	91.4	6.7	581	5 BP255845
C 13	91.4	6.7	582	5 BP234298
C 14	91.4	6.7	585	5 BP242668
C 15	91.4	6.7	598	7 CN283566
C 16	91.4	6.7	629	4 BG30559
C 17	91.4	6.7	633	2 BE313171
C 18	91.4	6.7	641	2 BE302648
C 19	91.4	6.7	666	6 CD68242
C 20	91.4	6.7	689	4 BG69621
C 21	91.4	6.7	693	5 BU623713
C 22	91.4	6.7	730	2 BU626230
C 23	91.4	6.7	753	4 BG622898
C 24	91.4	6.7	754	4 BG696675

ALIGNMENTS
RESULT 1 BU745135/c LOCUS BU745135 Canine heart non-normalized cDNA library in mRNA DEFINITION CHI#007_D09T3 Canine heart non-normalized cDNA clone CHI#007_D09 3', mRNA PRBLUESCRIPT SEQUENCE BU745135 VERSION BU745135.1 GI:23694297 KEYWORDS EST SOURCE ORGANISM Canis familiaris (dog) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. REFERENCE 1 (bases 1 to 819) AUTHORS Yi.Y., Dosei.R., Olarte.M., Henthorn.P. and George A.L. TITLE JOURNAL Unpublished (2003) COMMENT Other ESTs: CHI#007_D09T7 Contact: George AL Division of Genetic Medicine Vanderbilt University 529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA Tel: 615 936 2660 Fax: 615 936 2661 Email: al.george@vanderbilt.edu Insert length: 1655 Std Error: 0.00 Seq primer: T3: ATTAACCTCACTAAAGGA High quality sequence start: 55 High quality sequence stop: 628. FEATURES source 1. 81 /organism="Canis familiaris" /mol_type="mRNA" /db_xref="taxon:9615" /clone="CHI#007_D09" /tissue_type="heart" /cell_type="heart" /dev_stage="mixed developmental stages (adult, 30 day - 40 day fetal)" /clone_lib="Canine heart non-normalized cDNA Library in PRBLUESCRIPT" /note="Organ: heart; Vector: PRBLUESCRIPT; Site 1: 5' of vector Note 1; Site 2: 3' of vector End; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library Construction: oligo-dT primed"

Copyright (C) 1993 - 2005 Compugen Ltd.

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model
Run on: May 27, 2005, 03:05:18 ; Search time 2408 Seconds
(without alignments)
3472.625 Million cell updates/sec

Title: US-10-054-534B-13
Scoring table: IDNRTY_NUC
Perfect score: 1362
Sequence: 1 atggccaggsgcaaaggc.....aggatctccggatgtaa 1362

Searched: 5700845 seqs. 3069779757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/us07_PUBCOMB.seq: *
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq: *
3: /cgn2_6/ptodata/2/pubpna/us05_PUBCOMB.seq: *
4: /cgn2_6/ptodata/2/pubpna/us05_PUBCOMB.seq: *
5: /cgn2_6/ptodata/2/pubpna/us07_PUBCOMB.seq: *
6: /cgn2_6/ptodata/2/pubpna/PCTRS_PUBCOMB.seq: *
7: /cgn2_6/ptodata/2/pubpna/us08_PUBCOMB.seq: *
8: /cgn2_6/ptodata/2/pubpna/us08_PUBCOMB.seq: *
9: /cgn2_6/ptodata/2/pubpna/us09_PUBCOMB.seq: *
10: /cgn2_6/ptodata/2/pubpna/us09_PUBCOMB.seq: *
11: /cgn2_6/ptodata/2/pubpna/us09_PUBCOMB.seq: *
12: /cgn2_6/ptodata/2/pubpna/us09_PUBCOMB.seq: *
13: /cgn2_6/ptodata/2/pubpna/us09_PUBCOMB.seq: *
14: /cgn2_6/ptodata/2/pubpna/us09_PUBCOMB.seq: *
15: /cgn2_6/ptodata/2/pubpna/us09_PUBCOMB.seq: *
16: /cgn2_6/ptodata/2/pubpna/us09_PUBCOMB.seq: *
17: /cgn2_6/ptodata/2/pubpna/us09_PUBCOMB.seq: *
18: /cgn2_6/ptodata/2/pubpna/us09_PUBCOMB.seq: *
19: /cgn2_6/ptodata/2/pubpna/us10_PUBCOMB.seq: *
20: /cgn2_6/ptodata/2/pubpna/us11_PUBCOMB.seq: *
21: /cgn2_6/ptodata/2/pubpna/us11_PUBCOMB.seq: *
22: /cgn2_6/ptodata/2/pubpna/us11_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1362	100.0	1362	Sequence 13, Appl
2	1362	100.0	1362	Sequence 13, Appl
3	1362	100.0	1362	Sequence 13, Appl
4	1362	100.0	1362	Sequence 13, Appl
5	641.6	47.1	1380	Sequence 7, Appl
6	342.8	25.2	1434	Sequence 3, Appl
7	342.8	25.2	1434	Sequence 3, Appl
8	273.6	20.1	1374	Sequence 25, Appl
9	260.6	19.1	8894	Sequence 124, Appl
10	259.6	19.1	1374	Sequence 3, Appl
11	259.6	19.1	1374	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-769-863-13

; Sequence 13, Application US/09769863

; Publication No. US2003015714A1

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Mukerji, Pradip

; APPLICANT: Huang, Yung-Sheng

; APPLICANT: Das, Tapas

; APPLICANT: Thurmond, Jennifer

; APPLICANT: Pereira, Sarette L.

; TITLE OF INVENTION: DESMURASE GENES AND USES THEREOF

; FILE REFERENCE: 6763, US O1

; CURRENT APPLICATION NUMBER: US/09/769, 863

; CURRENT FILING DATE: 2001-01-25

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 13

; LENGTH: 1362

; TYPE: DNA

; ORGANISM: Saprolegnia diclina

; US-09-769-863-13

Query Match Score 100.0%; Score 1362; DB : Best Local Similarity 100.0%; Pred. No. 0; Matches 1362; Conservative 0; Mismatches 6

Ory 1 ATGGTCGAGGCCAAAGCCGAGATCTCTGGGT

Db 1 ARGGTCGAGGCCAAAGCCGAGATCTCTGGGT

61 CAGACGACGCGTGGATGTTGATCCACCAAGGTG

61 CAGACGACGCGTGGATGTTGATCCACCAAGGTG

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

```
description
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 35, Appl
Sequence 7, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 25, Appl
Sequence 124, Appl
Sequence 3, Appl
Sequence 1, Appl
```

GenCore Version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: May 27, 2005, 00:54:26 ; Search time 264 Seconds
 (without alignments)
 8441.700 Million cell updates/sec

Title: US-10-054-534-B-13
 Perfect score: 1362
 Sequence: 1 atggcccgaggcaaaagc.....aggagtttccggccatgtaa 1362
 Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents NA:
 1: /cgn2_6/pctodata/1/ina/5A_COMB.seq: *
 2: /cgn2_6/pctodata/1/ina/5B_COMB.seq: *
 3: /cgn2_6/pctodata/1/ina/6A_COMB.seq: *
 4: /cgn2_6/pctodata/1/ina/6B_COMB.seq: *
 5: /cgn2_6/pctodata/1/ina/PCTUS_COMB.seq: *
 6: /cgn2_6/pctodata/1/ina/backfilesl.seq: *

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1362	100.0	1362	4	US-09-769-863-13	Sequence 13; Appl
2	259.6	19.1	1617	2	US-08-834-655-1	Sequence 1; Appl
3	259.6	19.1	1617	3	US-08-834-033A-1	Sequence 1; Appl
4	259.6	19.1	1617	3	US-05-363-574-1	Sequence 1; Appl
5	259.6	19.1	1617	3	US-09-330-235-17	Sequence 17; Appl
6	259.6	19.1	1617	3	US-09-330-235-17	Sequence 17; Appl
7	100.6	7.4	1281	4	US-09-857-583B-3	Sequence 3; Appl
8	91.4	6.7	1686	3	US-09-433-261-6	Sequence 6; Appl
9	91.4	6.7	1686	3	US-09-227-613-6	Sequence 6; Appl
10	91.4	6.7	1843	3	US-09-433-261-7	Sequence 7; Appl
11	91.4	6.7	1843	3	US-09-433-261-7	Sequence 7; Appl
12	91.4	6.7	2257	3	US-09-439-261-8	Sequence 8; Appl
13	91.4	6.7	2257	3	US-09-227-613-8	Sequence 8; Appl
14	91.4	6.7	2540	4	US-09-223-655-295	Sequence 295; Appl
15	91.4	6.7	3158	4	US-09-949-016-4613	Sequence 4613; Appl
16	89.6	6.6	1717	4	US-09-048-888-2	Sequence 2; Appl
17	89.6	6.6	1758	4	US-09-949-016-4904	Sequence 4904; Appl
18	85.8	6.3	347	4	US-09-702-705-355	Sequence 355; Appl
19	85.8	6.3	347	4	US-09-736-457-355	Sequence 355; Appl
20	85.8	6.3	347	4	US-09-614-124B-355	Sequence 355; Appl
21	85.8	6.3	347	4	US-09-671-325-355	Sequence 355; Appl
22	85.8	6.3	347	4	US-09-184-355	Sequence 355; Appl
23	85.8	6.3	347	4	US-09-589-824-355	Sequence 355; Appl
24	77.6	5.7	1478	4	US-09-148-545-63	Sequence 63; Appl
25	77.6	5.7	2016	4	US-09-148-545-119	Sequence 119; Appl
26	5.2	1320	4	US-09-763-28	Sequence 28; Appl	
27	4.8	1702	3	US-08-934-254-26	Sequence 26; Appl	

ALIGNMENTS

RESULT 1
 US-09-769-863-13
 Sequence 13; Application US/09769863
 Sequence No. 6633451
 GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories **Abbott**
 APPLICANT: Mukerji, Pradip
 APPLICANT: Huang, Yung-Sheng
 APPLICANT: Dab, Tapas
 APPLICANT: Thurmond, Jennifer
 APPLICANT: Zareira, Suzette L.
 TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
 CURRENT APPLICATION NUMBER: US/09/769,863
 CURRENT FILING DATE: 2001-01-25
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FabSEQ for Windows Version 4.0
 SEQ ID NO 13
 LENGTH: 1362
 TYPE: DNA
 ORGANISM: Saprolegnia diclina
 US-09-769-863-13

Query Match 100.0%; Score 1362; DB 4; Length 1362;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCCCGAGGCGAAAGGCCGAGAAGATCTGGCGGCACATCCGCGAGGCAACGC 60
 Db 1 ATGGCTCAGGGCGAAAGCCGAGAAGATCTGGCGGCACATCCGCGAGGCAACGC 60
 Qy 61 CAACGACAAAGCGTGTGATGTGTCACCAACAGGTAGAGAACATCTCGCCATTGAGAC 120
 Db 61 CAACGACAAAGCGTGTGATGTGTCACCAACAGGTAGAGAACATCTCGCCATTGAGAC 120
 Qy 121 CACCCGCGCGCGCTGATGTCACCGGGGGAGAGCCGACCGATGTTCTCTGAGAC 180
 Db 121 CACCCGCGCGCGCTGATGTCACCGGGGGAGAGCCGACCGATGTTCTCTGAGAC 180
 Qy 181 GTCCTCCACCCGAGCTCGCGCTCAAGCTCTCGAGCTGACTACGTTGGCGCGCTGCGAC 240
 Db 181 GTCCTCCACCCGAGCTCGCGCTCAAGCTCTCGAGCTGACTACGTTGGCGCGCTGCGAC 240
 Qy 241 CAGTCGACGCCCGCGCTGACAGCTGTCAGGAGGTCAGAGAGCGCTGCGAC 300
 Db 241 CAGTCGACGCCCGCGCTGACAGCTGTCAGGAGGTCAGAGAGCGCTGCGAC 300
 Qy 301 TCTATTCGCTTACCCGAAAGTGGCGCTGAGTCAGGCGCTGAGCTGAGCTGCGAC 360
 Db 301 TCTATTCGCTTACCCGAAAGTGGCGCTGAGTCAGGAGGTCAGGCTGAGCTGAGCTGCGAC 360

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using BW model

Run on:

May 26, 2005, 23:08:41 ; Search time 820 Seconds
(without alignments)
9832.546 Million cell updates/sec

Title: US-10-054-534B-13

Perfect score: 1362

Sequence: I atggtcacggggcaaaaggc.....aggagtcccgccatgtaa 1362

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cb:*

11: geneseqn2003db:*

12: geneseqn2004aa:*

13: geneseqn2004ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1362	100.0	1362	8	ADR49064	Ad49064 Saprolegnia Adr20162 Saprolegnia
2	1362	100.0	1362	13	ADR20162	Adr20162 Saprolegnia
3	641.6	47.1	1380	6	AD35090	Ad35090 Pythium i
4	342.8	25.2	1434	6	ABV74258	Abv74258 Phaeodact
5	342.8	25.2	1434	6	ABD76780	Abq7788 P. tricorn
6	342.8	25.2	1443	13	ADR49337	Adr49337 Phaeodact
7	25.2	17061	13	ADR49339	Adr49339 Phaeodact	
8	259.6	19.1	1374	3	ADZ47129	Adz47129 Fungal de
9	259.6	19.1	1617	2	AMV63624	Aav63624 cDNA enco
10	259.6	19.1	1617	2	AAX00889	Aax00889 Mortierell
11	259.6	19.1	1617	3	AAG09430	Aaa0943 M. alpina
12	259.6	19.1	1617	12	ADF89558	Adf89558 M. alpina
13	259.6	19.1	1617	13	ADR20160	Adr20160 Mortierell
14	258.4	19.0	1374	5	AFB25234	Aaf25234 Nucleocid
15	149.6	11.0	648	6	ABV74268	Abv74268 Phaeodact
16	149.6	11.0	648	6	ABG76790	Abg76790 P. tricorn
17	129.5	9.5	1404	8	ABV76916	Abv7691 Nucleotid
18	107.2	7.9	2054	12	ADJ48284	Adj48284 Maize oil
19	106.2	7.8	2160	4	AFB25734	Aaf25734 C. purpur
20	100.6	7.4	1275	3	AAA51233	Aaa51233 E. gracil

POST-PROCESSING

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cb:*

11: geneseqn2003db:*

12: geneseqn2004aa:*

13: geneseqn2004ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

POST-PROCESSING

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cb:*

11: geneseqn2003db:*

12: geneseqn2004aa:*

13: geneseqn2004ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

POST-PROCESSING

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cb:*

11: geneseqn2003db:*

12: geneseqn2004aa:*

13: geneseqn2004ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

POST-PROCESSING

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cb:*

11: geneseqn2003db:*

12: geneseqn2004aa:*

13: geneseqn2004ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

POST-PROCESSING

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cb:*

11: geneseqn2003db:*

12: geneseqn2004aa:*

13: geneseqn2004ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

POST-PROCESSING

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cb:*

11: geneseqn2003db:*

12: geneseqn2004aa:*

13: geneseqn2004ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

POST-PROCESSING

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cb:*

11: geneseqn2003db:*

12: geneseqn2004aa:*

13: geneseqn2004ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

POST-PROCESSING

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cb:*

11: geneseqn2003db:*

12: geneseqn2004aa:*

13: geneseqn2004ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

POST-PROCESSING

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cb:*

11: geneseqn2003db:*

12: geneseqn2004aa:*

13: geneseqn2004ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

POST-PROCESSING

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cb:*

11: geneseqn2003db:*

12: geneseqn2004aa:*

13: geneseqn2004ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

POST-PROCESSING

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:

Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2005, 00:04:07 ; Search time 6:176 Seconds
 (Without alignments)

10685.881 Million cell updates/sec

Title: US-10-054-534B-13

Perfect score: 1362

Sequence: 1 atggtcacaggcaaaaggc.....aggagttcccgccatgtaa 1362

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBmbl:
 1: gb_ba::*
 2: gb_hg::*
 3: gb_in::*
 4: gb_on::*
 5: gb_ov::*
 6: gb_pt::*
 7: gb_ph::*
 8: gb_pr::*
 9: gb_pc::*
 10: gb_pj::*
 11: gb_sb::*
 12: gb_sy::*
 13: gb_ln::*
 14: gb_v1::*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1362	100.0	1362	AR410195
2	1362	100.0	1362	AR410195
3	641.6	47.1	1380	AR419296
4	641.6	47.1	1380	AR419296
5	342.8	25.2	1434	AR481613
6	342.8	25.2	1434	AR481942
7	342.8	25.2	1434	AR491573
8	342.8	25.2	1443	AR082393
9	342.8	25.2	17061	CQB74879
10	342.8	25.2	17061	AB020032
11	260.8	19.1	1590	AB070557
12	260.8	19.1	2207	Mortierel
13	259.6	19.1	1374	BD232180
14	259.6	19.1	1617	AR080598
15	259.6	19.1	1617	AR09439
16	259.6	19.1	1617	AR136018
17	259.6	19.1	1617	AR215236
18	259.6	19.1	1617	AR235375
19	259.6	19.1	1617	BD082621

LISTINGS

Database :

GenBmbl:

Listing first 45 summaries

ALIGMENTS

Database :

GenBmbl:

Listing first 45 summaries

RESULTS

Database :

GenBmbl:

Listing first 45 summaries

REFINEMENT

Database :

GenBmbl:

Listing first 45 summaries

PATENTS

Database :

GenBmbl:

Listing first 45 summaries

SEQUENCES

Database :

GenBmbl:

Listing first 45 summaries

STRUCTURES

Database :

GenBmbl:

Listing first 45 summaries

ORGANISMS

Database :

GenBmbl:

Listing first 45 summaries

KEYWORDS

Database :

GenBmbl:

Listing first 45 summaries

VERSION

Database :

GenBmbl:

Listing first 45 summaries

ACCESION

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

SEQUENCE

Database :

GenBmbl:

Listing first 45 summaries

VERSION

Database :

GenBmbl:

Listing first 45 summaries

ACCESION

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl:

Listing first 45 summaries

DEFINITION

Database :

GenBmbl:

Listing first 45 summaries

LOCUS

Database :

GenBmbl: